

(FILE 'HOME' ENTERED AT 10:40:17 ON 13 JUL 2003

FILE 'REGISTRY' ENTERED AT 10:40:30 ON 13 JUL 2003

L1 44 S CC.{4}C.Y.C/SQSP

FILE 'CA' ENTERED AT 10:44:44 ON 16 JUL 2003

L2 25 S L1

L3 5 S CONOTOXIN AND L2

L2 ANSWER 1 OF 25 CA COPYRIGHT 2003 ACS

T1 Human colon and colon cancer-associated polynucleotides and polypeptides and their diagnostic and therapeutic applications

PY 2003

2001

2003

L2 ANSWER 2 OF 25 CA COPYRIGHT 2003 ACS

T1 DNA and protein sequences of human hair keratin-associated proteins and their used

PY 2003

L2 ANSWER 3 OF 25 CA COPYRIGHT 2003 ACS

T1 Polymorphisms in the human high sulfur hair keratin-associated protein 1, KAP1, gene family

PY 2002

L2 ANSWER 4 OF 25 CA COPYRIGHT 2003 ACS

T1 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

PY 2002

L2 ANSWER 5 OF 25 CA COPYRIGHT 2003 ACS

T1 Novel conotoxins for use in the therapeutic regulation of ion channel function

PY 2002

2003

2003

L2 ANSWER 6 OF 25 CA COPYRIGHT 2003 ACS

T1 Identification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells

PY 2002

L2 ANSWER 7 OF 25 CA COPYRIGHT 2003 ACS

T1 Nucleic acids and their encoded polypeptides from human tissues

PY 2001

2001

L2 ANSWER 8 OF 25 CA COPYRIGHT 2003 ACS

T1 Human nucleic acids and polypeptides and their diagnostic and therapeutic uses

PY 2001

2001

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2002

L2 ANSWER 9 OF 25 CA COPYRIGHT 2003 ACS

T1 Reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes

PY 2001

2001

2003

L2 ANSWER 10 OF 25 CA COPYRIGHT 2003 ACS

T1 Complete genome sequence of the shrimp white spot bacilliform virus

PY 2001

L2 ANSWER 11 OF 25 CA COPYRIGHT 2003 ACS

T1 New members of the .mu.-conotoxin family for use in the treatment of disease associated with sodium channel function and cDNAs encoding them

PY 2002

2002

2003

L2 ANSWER 12 OF 25 CA COPYRIGHT 2003 ACS

T1 Characterization of a cluster of human high/ultrahigh sulfur keratin-associated protein genes embedded in the type I keratin gene domain on chromosome 17q12-21

PY 2001

L2 ANSWER 13 OF 25 CA COPYRIGHT 2003 ACS

T1 Nucleic acids and their encoded polypeptides from human tissues

PY 2001

L2 ANSWER 14 OF 25 CA COPYRIGHT 2003 ACS

T1 Mechanisms for evolving hypervariability: the case of conopeptides

PY 2001

L2 ANSWER 15 OF 25 CA COPYRIGHT 2003 ACS

T1 An efficient synthetic scheme for natural .alpha.-conotoxins and their analogues

PY 2001

L2 ANSWER 16 OF 25 CA COPYRIGHT 2003 ACS

T1 Colon and colon cancer associated cDNAs and proteins and their use in diagnosis and treatment of colon cancer

PY 2001

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2003

L2 ANSWER 17 OF 25 CA COPYRIGHT 2003 ACS

T1 Functional annotation of a full-length mouse cDNA collection

PY 2001

L2 ANSWER 18 OF 25 CA COPYRIGHT 2003 ACS

T1 Alpha-conotoxins and nucleic acids encoding them

PY 2000

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2002

L2 ANSWER 19 OF 25 CA COPYRIGHT 2003 ACS

T1 Human and murine secreted proteins and nucleic acids encoding them

PY 2000

2001

L2 ANSWER 20 OF 25 CA COPYRIGHT 2003 ACS

T1 The genome sequence of Drosophila melanogaster

PY 2000

L2 ANSWER 21 OF 25 CA COPYRIGHT 2003 ACS

T1 Cloning of human epidermal proteins HEPI-1 to HEPI-6 and their cDNA sequences and diagnostic and therapeutic applications

PY 2000

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2003

L2 ANSWER 22 OF 25 CA COPYRIGHT 2003 ACS

T1 RNA editing in the free-living bodonid Bodo saltans. [Erratum to document cited in CA129:1279]

PY 1998

L2 ANSWER 23 OF 25 CA COPYRIGHT 2003 ACS

T1 RNA editing in the free-living bodonid Bodo saltans

PY 1998

L2 ANSWER 24 OF 25 CA COPYRIGHT 2003 ACS

T1 Structure and hair follicle-specific expression of genes encoding the rat high sulfur protein B2 family

PY 1998

L2 ANSWER 25 OF 25 CA COPYRIGHT 2003 ACS

T1 Cloning and structural characterization of human hair high-sulfur keratin genes

PY 1992

ANSWER 1 OF 5 CA COPYRIGHT 2003 ACS

T1 Novel conotoxins for use in the therapeutic regulation of ion channel function

PY 2002

2003

2003

L3 ANSWER 2 OF 5 CA COPYRIGHT 2003 ACS

T1 New members of the .mu.- ***conotoxin*** family for use in the treatment of disease associated with sodium channel function and cDNAs encoding them

PY 2002

2002
2003

L3 ANSWER 3 OF 5 CA COPYRIGHT 2003 ACS

TI Mechanisms for evolving hypervariability: the case of conopeptides
PY 2001

L3 ANSWER 4 OF 5 CA COPYRIGHT 2003 ACS

TI An efficient synthetic scheme for natural .alpha.-conotoxins and their
analogues
PY 2001

L3 ANSWER 5 OF 5 CA COPYRIGHT 2003 ACS

TI Alpha-conotoxins and nucleic acids encoding them
PY 2000
2001
2002

L4 ANSWER 1 OF 1 CA COPYRIGHT 2003 ACS

AN 119:87666 CA

TI Cloning and structural characterization of human hair high-sulfur keratin
genes

AU Zhumabaeva, B. D.; Gening, L. V.; Gazaryan, K. G.

CS Inst. Mol. Genet., Moscow, 123182, Russia

SO Molekulyarnaya Biologiya (Moscow) (1992), 26(4), 813-20

CODEN: MOBIBO; ISSN: 0026-8984

DT Journal

LA Russian

L2 ANSWER 23 OF 25 CA COPYRIGHT 2003 ACS

AN 129:1279 CA

TI RNA editing in the free-living bodonid Bodo saltans

AU Blom, Daniel; De Haan, Annett; Van Den Berg, Marlene; Sloof, Paul; Jirku,
Milan; Lukes, Julius; Benne, Rob

CS Department of Biochemistry/AMC, University of Amsterdam, Amsterdam, 1105

AZ, Neth.

SO Nucleic Acids Research (1998), 205-1213

CODEN: NARHAD; ISSN: 0305-1048

PB Oxford University Press

DT Journal

LA English

AB In parasitic kinetoplastid protozoa, mitochondrial (mt) mRNAs are post-transcriptionally edited by insertion and deletion of uridylylate residues, the information being provided by guide (g) RNAs. In order to further explore the role and evolutionary history of this process, we searched for editing in mt RNAs of the free-living bodonid Bodo saltans. We found extensive editing in the transcript for NADH dehydrogenase (ND) subunit 5, which is unedited in trypanosomatids. In contrast, B. saltans cytochrome c oxidase (cox) subunit 2 and maxicircle unidentified reading frame (MURF) 2 RNAs display limited editing in the same regions as their trypanosomatid counterparts. A putative intramol. cox2 gRNA and the gene for gMURF2-1 directing the insertion of only one U in the 5' editing domain of MURF2 RNA, are conserved in B. saltans. This lends (further) evolutionary support to the proposed role of these sequences as gRNAs. Phylogenetic anal. showed that B. saltans is more closely related to trypanosomatids than the cryptobionts Trypanoplasma borreli and Cryptobia helicis, in line with the trypanosomatid-like cox2 and MURF2 RNA editing patterns. Nevertheless, other features like the apparent absence of a catenated mtDNA network, are shared with bodonid and cryptobiont species. ND5 RNA editing may represent yet another example of editing 'on the way out' during kinetoplastid evolution, but in view of the fact that cox2 RNA is unedited in T. borreli and C. helicis, we infer that the editing of this RNA may have arisen relatively recently. Our results provide the first examples of RNA editing in a free-living kinetoplastid, indicating that there is no direct link between U-insertion/deletion editing and a parasitic lifestyle.

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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 14 OF 25 CA COPYRIGHT 2003 ACS

AN 135:222087 CA

TI Mechanisms for evolving hypervariability: the case of conopeptides

AU Conticello, Silvestro G.; Gilad, Yoav; Avidan, Nili; Ben-Asher, Edna; Levy, Zehava; Fainzilber, Mike

CS Laboratory of Molecular Neurobiology, Department of Biological Chemistry, Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, 76100, Israel

SO Molecular Biology and Evolution (2001), 18(2), 120-131

CODEN: MBEVEO; ISSN: 0737-4038

PB Society for Molecular Biology and Evolution

DT Journal

LA English

AB Hypervariability is a prominent feature of large gene families that mediate interactions between organisms, such as venom-derived toxins or Igs. In order to study mechanisms for evolution of hypervariability, we examd. an EST-generated assemblage of 170 distinct conopeptide sequences from the venoms of five species of marine *Conus* snails. These sequences were assigned to eight gene families, defined by conserved elements in the signal domain and untranslated regions. Order-of-magnitude differences were obsd. in the expression levels of individual conopeptides, with five to seven transcripts typically comprising over 50% of the sequenced clones in a given species. The conopeptide precursor alignments revealed four striking features peculiar to the mature peptide domain: (1) an accelerated rate of nucleotide substitution, (2) a bias for transversions over transitions in nucleotide substitutions, (3) a position-specific conservation of cysteine codons within the hypervariable region, and (4) a preponderance of nonsynonymous substitutions over synonymous substitutions. We propose that the first three observations argue for a mutator mechanism targeted to mature domains in conopeptide genes, combining a protective activity specific for cysteine codons and a mutagenic polymerase that exhibits transversion bias, such as DNA polymerase V. The high Dn/Ds ratio is consistent with pos. or diversifying selection, and further analyses by intraspecific/interspecific gene tree contingency tests weakly support recent diversifying selection in the evolution of conopeptides. Since only the most highly expressed transcripts segregate in gene trees according to the feeding specificity of the species, diversifying selection might be acting primarily on these sequences. The combination of a targeted mutator mechanism to generate high variability with the subsequent action of diversifying selection on highly expressed variants might explain both the hypervariability of conopeptides and the large no. of unique sequences per species.

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